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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter

Sequence 1 |cl|seq\_1 Length 510 (1 .. 510)

Sequence 2 |cl|seq\_2 Length 512 (1 .. 512)

2

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 786 bits (2029), Expect = 0.0  
Identities = 419/522 (80%), Positives = 448/522 (85%), Gaps = 22/522 (4%)

Query: 1 MFIESFRVESPHVRYGAAEIESDYQYDTTELVHESHDGASRWIVRPKSVRYNFRTTTTVP  
60 MFIESFRVESPHVRYGAAEIES+Y+YDTTELVHESHDGASRW+VRPKSV+Y+FRT+TTVP  
Sbjct: 1 MFIESFRVESPHVRYGAAEIESEYRYDTTELVHESHDGASRWVVRPKSVQYHFRSTTTVP  
60  
Query: 61 KLGVMLVGWGGNNNGSTLTAGVIANREGISWATKDKVQQANYYGSLTQASTIRVGSYNGEE  
120 KLGVMLVGWGGNNNGSTLTAGVIA+REGISWATKDKVQQANYYGSLTQASTIRVGSYNGEE  
Sbjct: 61 KLGVMLVGWGGNNNGSTLTAGVIASREGISWATKDKVQQANYYGSLTQASTIRVGSYNGEE  
120  
Query: 121 IYAPFKSLLPMVNPDVLVFGWDISNMNLADAMTRAKVLDIDLQKQLRPYME-----  
173 IYAPFKSLLPMVNPDDEVFGWDISNMNLADAMTRAKVLDIDLQKQLRPYME  
Sbjct: 121 IYAPFKSLLPMVNPDVLVFGWDISNMNLADAMTRAKVLDIDLQKQLRPYMEWCLSLAS  
180  
Query: 174 MVPL--PGIYDPDVIAANQGSRANNVIKGTKKEQMEQIIKDIREFKEKSVDKVVVLWTA  
231 M+P P DP A SR ++ + + KDIREFKE IK+DK VVI.WTA  
Sbjct: 181 MPTSSPLTRDP---ARTMSSRE-----PRRSRWGRSSKDIREFKENNKMOKAVVI.WTA  
231

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Fig: 1

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Query: 232 NTERYSN-VCVGLNDTMENLLASVDKNEAEISPSTLYAICV-MEGIPEFINGSQNTFVP  
289

NTERY+N I C+GI T ASVD+N+AEISPSTLY I EG+ I G+ + P

Sbjct: 232 NTERYNMCLCLGLM-TNGKPSASVDRNQAEISPSTLYCHCLASL&GVRASITGALKKKSWP  
290

Query: 290 GLIDLAIKNCLI-GGDDFKSGQTKMKSVLVDLFLVGAGIKPTSIVSYNHGNNGMNLSA  
348

G+ DLAIK GG K G+ K K+ LVDFL+GAGIKPTSIVSYNHGNNDG NLSA

Sbjct: 291 GIDDLAIKKKLDPGGLIQQKRGKPKKKTGLVDLFLMGAGIKPTSIVSYNHGNNDGTLNLSA  
350

Query: 349 PQTFRSKEISKSNVVDDMVSSNAILYELGEHPDHVVVIKYVVPYVGDSKRAMDEYTSEIFM  
408

PQTFRSKEISK+VVDDMVSSNAILYE GEHPDHVVVIKYVVPYVGDSKRAMDEYTSEIFM

Sbjct: 351 PQTFRSKEISKSSVVDDMVSSNAILYEPGEHPDHVVVIKYVVPYVGDSKRAMDEYTSEIFM  
410

Query: 409 GGKSTIVLHNTCEDSLLAAPIIILDLVLLAELSTRIQLKAEGEKFHSFHPVATILSYLTK  
468

GGK+TIVLHNTCEDSLLAAPIIILDLVLLAELSTRIQLK EGEKEKFHSFHPVATILSYLTK

Sbjct: 411 GGKNTIVLHNTCEDSLLAAPIIILDLVLLAELSTRIQLKGEGEKFHSFHPVATILSYLTK  
470

Query: 469 APLVPPGTPVNVNALAKQRAMLENIMRACVGLAPENNMLEYK 510.  
APLVPPGTPVNVNALAKQRAMLENIMRACVGLAPENNMLEYK

Sbjct: 471 APLVPPGTPVNVNALAKQRAMLENIMRACVGLAPENNMLEYK 512

CPU time: 0.10 user secs. 0.02 sys. secs 0.12 total  
secs.

## Gapped

Lambda	K	H
0.316	0.134	0.385

## Gapped

Lambda	K	H
0.267	0.0410	0.140

## Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 2125

Number of Sequences: 0

Number of extensions: 153

Number of successful extensions: 5

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 510

length of database: 233,319,389

effective HSP length: 125

effective length of query: 385

effective length of database: 176,133,389

effective search space: 67811354765

effective search space used: 67811354765

Fig : 1 (cont'd)

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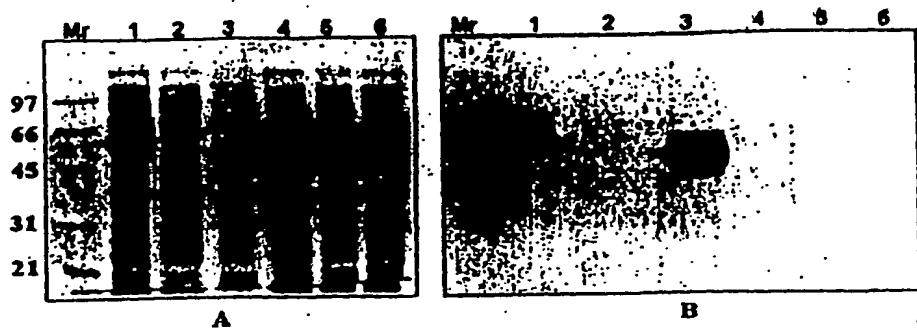


Fig. 2

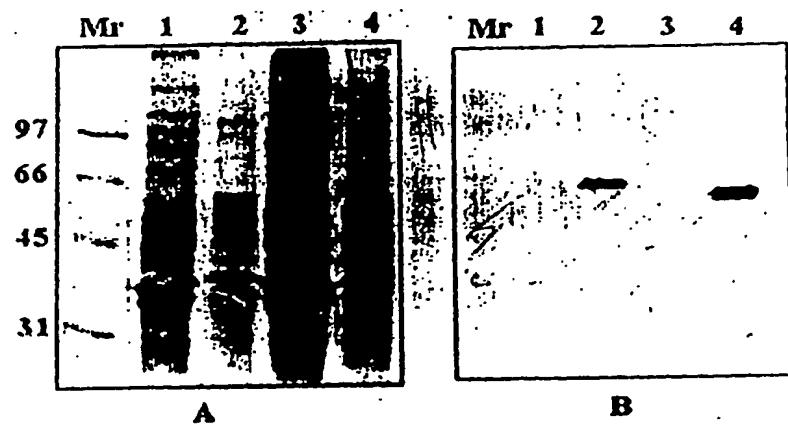


Fig. 3

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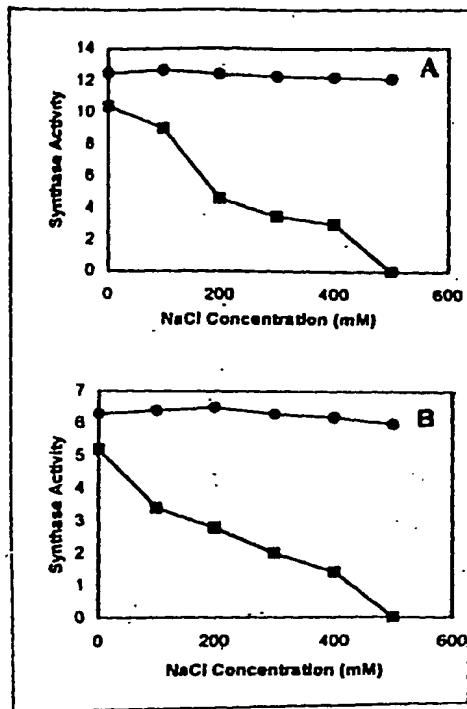


Fig : 4

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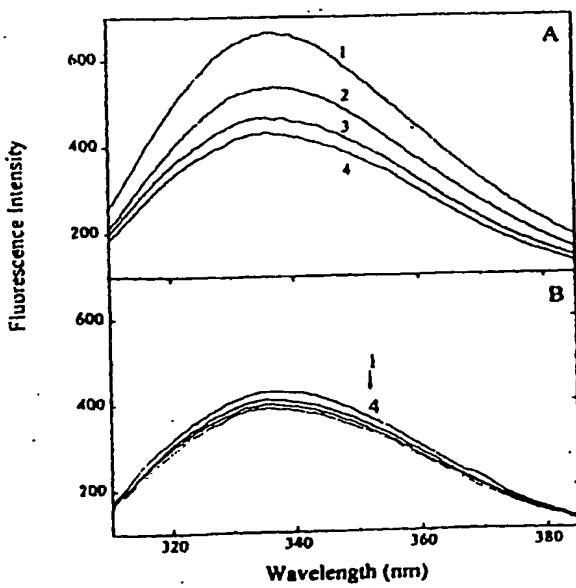


Fig. 5

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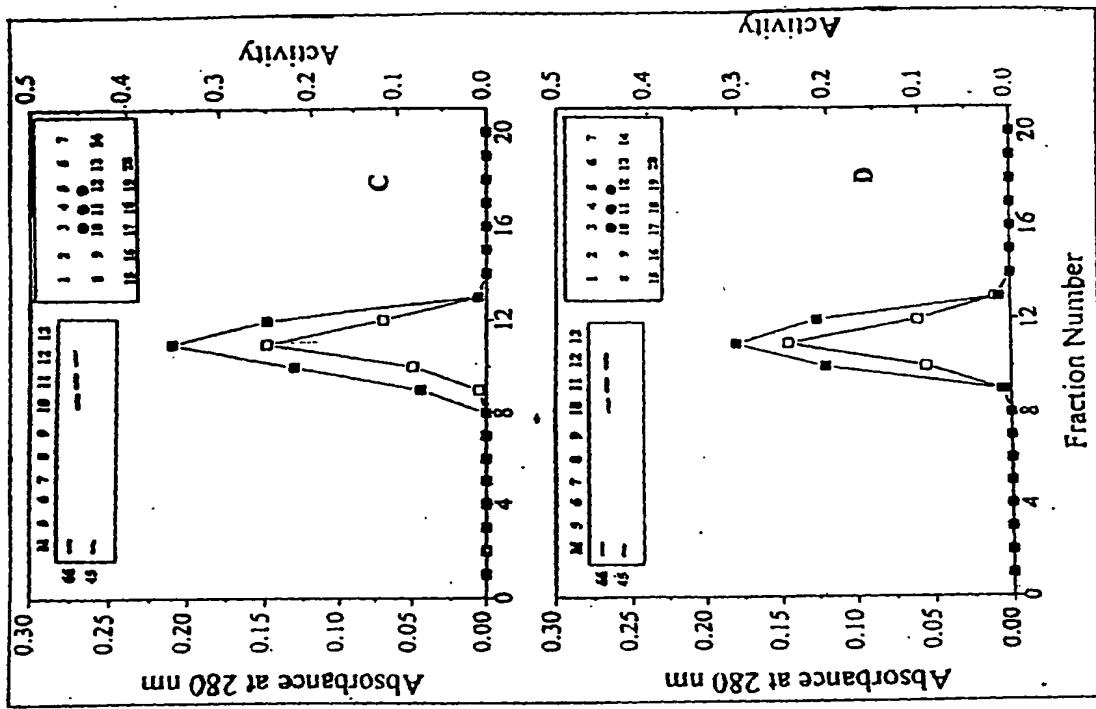
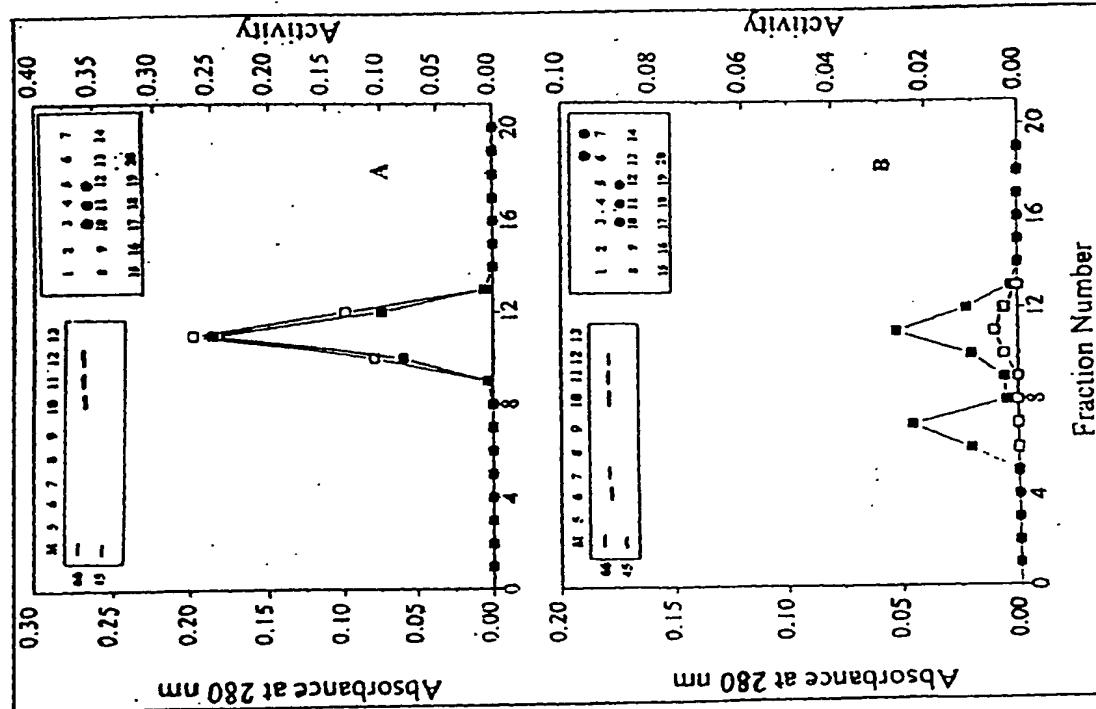


Fig. 6



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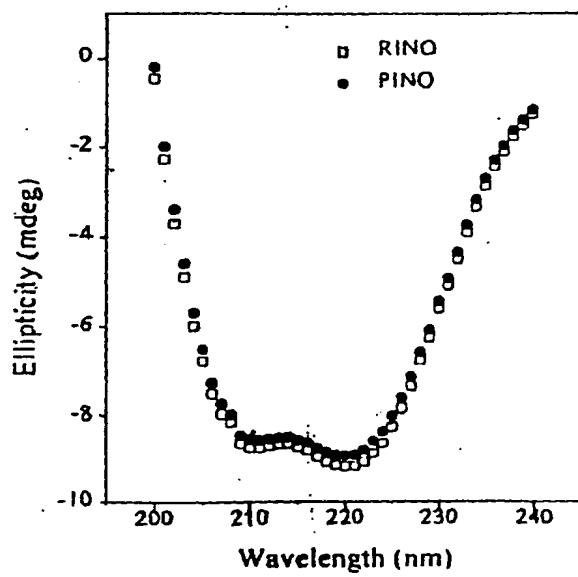


Fig : 7

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